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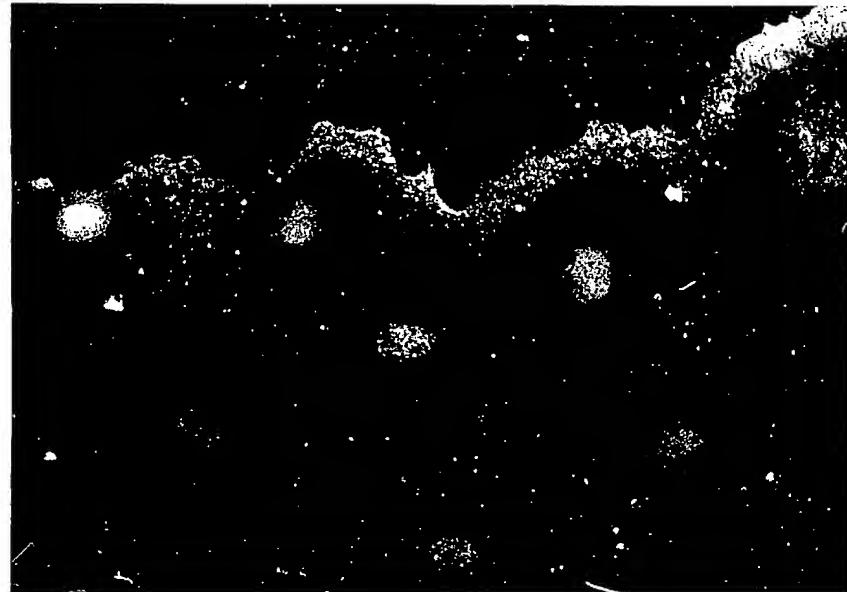


Fig. 1

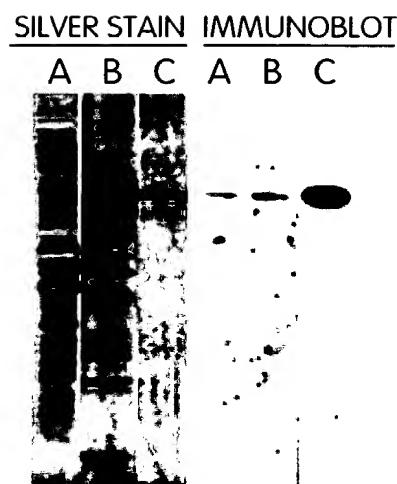


Fig. 2



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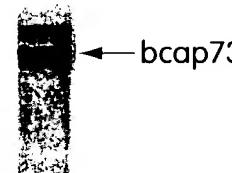


Fig. 3A

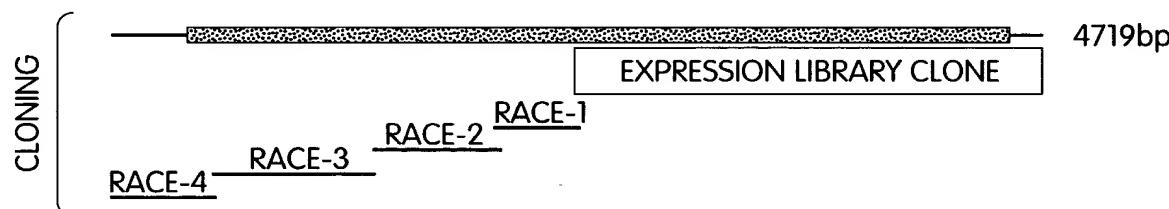


Fig. 3B

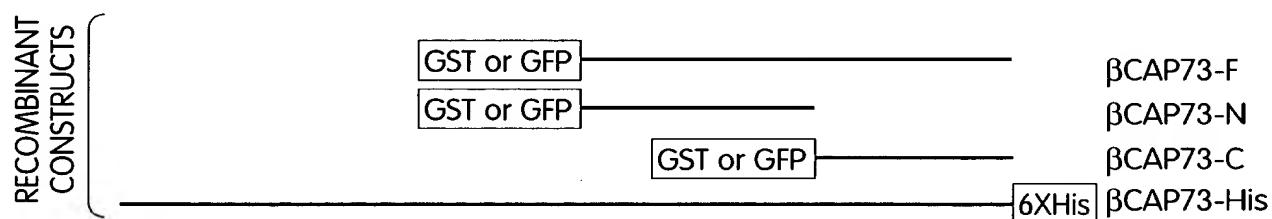


Fig. 3C



Fig. 3D



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cagtgtttag gccccaggat gtagagtgttcaagctt tccagtggag tccccaaaa 60
 gggaggcag agaaagacat cttctaaata acaaatacgat ggagttacag tacctgactt 120
 ggggctgctc ttaatcaagt gctgccgtg caaggaagat aattttcaag cgttatgaag 180
 gcggagaagg attccgaaga cgaagaaaat atccttagag atccaagcta agtgttagtgc 240
 agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtca ctagtttagga 300
 gtctctctga gggctggctt tgtgagccac agtgattgt aacttaatgc gaactaattt 360
 gctgttagca acaagaaaact aaatcctgtc t atg atg agc tgt tgg ttt tct 412
 Met Met Ser Cys Trp Phe Ser
 1 5

tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac 460
 Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp
 10 15 20

cga ttg atg aga gca gca gaa agg gga gat gta gaa aaa gtg tcc tca 508
 Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser
 25 30 35

atc ctt gct aaa aag gga gtc aat cca ggc aag cta gat gta gaa ggc 556
 Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly
 40 45 50 55

aga tct gcc ttt cat gtt gtg gcc tca aag gga aat ctt gag tgt ttg 604
 Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu
 60 65 70

aat gcc atc ctc ata cat gga gtt gat att aca acc agt gac acc gca 652
 Asn Ala Ile Leu Ile His Gly Val Asp Ile Thr Ser Asp Thr Ala
 75 80 85

gga agg aat gct ctt cac ctg gct gca aag tat ggg cat gca ctg tgt 700
 Gly Arg Asn Ala Leu His Leu Ala Ala Lys Tyr Gly His Ala Leu Cys
 90 95 100

cta caa aaa ctt cta cag tac aat tgt ccc act gaa cat gta gac ctg 748
 Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro Thr Glu His Val Asp Leu
 105 110 115

cag gga aga act gca ctt cat gat gca gct atg gca gac tgt cct tct 796
 Gln Gly Arg Thr Ala Leu His Asp Ala Ala Met Ala Asp Cys Pro Ser
 120 125 130 135

agc ata cag ctg ctc tgc gac cat ggg gcc tcg gtg aat gcc aaa gat 844
 Ser Ile Gln Leu Leu Cys Asp His Gly Ala Ser Val Asn Ala Lys Asp
 140 145 150

Fig. 4-1



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gta gat ggg cg	aca cca ctt gtt ctg gct acc cag atg tgt agg cca	892	
Val Asp Gly Arg	Thr Pro Leu Val Leu Ala Thr Gln Met Cys Arg Pro		
155	160	165	
aca ata tgt caa ctg ctg ata gat aga ggg gcg gat att aat tcc aga	940		
Thr Ile Cys Gln Leu Leu Ile Asp Arg Gly Ala Asp Ile Asn Ser Arg			
170	175	180	
gac aaa caa aac agg act gct ctc atg cta gga tgc gag tat ggt tgc	988		
Asp Lys Gln Asn Arg Thr Ala Leu Met Leu Gly Cys Glu Tyr Gly Cys			
185	190	195	
aaa gat gca gta gaa gtc tta atc aaa aac ggc gct gac gtg acc ttg	1036		
Lys Asp Ala Val Glu Val Leu Ile Lys Asn Gly Ala Asp Val Thr Leu			
200	205	210	215
ctg gac gcc ctt ggc cat gac agt tct tac tat gca aga att ggt gac	1084		
Leu Asp Ala Leu Gly His Asp Ser Ser Tyr Tyr Ala Arg Ile Gly Asp			
220	225	230	
aat ctg gac att cta acc tta ctg aag act gca tca gaa aat tcc aac	1132		
Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr Ala Ser Glu Asn Ser Asn			
235	240	245	
aaa ggg aga gaa ctt tgg aag aaa gga cca tct tta caa cag cga aat	1180		
Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro Ser Leu Gln Gln Arg Asn			
250	255	260	
ttg tct cag atg cta gat gaa gta aat acg aag tca aat cag agg gag	1228		
Leu Ser Gln Met Leu Asp Glu Val Asn Thr Lys Ser Asn Gln Arg Glu			
265	270	275	
cat caa aac att cag gat ctg gag att gaa aat gaa gat ctg aaa gag	1276		
His Gln Asn Ile Gln Asp Leu Glu Ile Glu Asn Glu Asp Leu Lys Glu			
280	285	290	295
aga ttg aga aaa att cag caa gaa cag aga ata tta ttg gat aaa gtc	1324		
Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg Ile Leu Leu Asp Lys Val			
300	305	310	
aat ggt tta cag cta cag ctg aat gag gaa gta atg gtg gct gat gat	1372		
Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu Val Met Val Ala Asp Asp			
315	320	325	
ctg gaa agt gag aaa gaa aag ctg aag tcc ctt ttg gca gcc aaa gaa	1420		
Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser Leu Leu Ala Ala Lys Glu			
330	335	340	
aag cag cat gaa gaa agc cta aga act att gag gct ctg aaa agt aga	1468		
Lys Gln His Glu Glu Ser Leu Arg Thr Ile Glu Ala Leu Lys Ser Arg			
345	350	355	

Fig. 4-2



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ttt aag tat ttt gag agt gat cat tta gga tca gga agt cat ttc agg Phe Lys Tyr Phe Glu Ser Asp His Leu Gly Ser Gly Ser His Phe Arg 360 365 370 375	1516
aaa gaa gat atg ctt ctt aaa caa ggt caa atg tac atg aca gac tca Lys Glu Asp Met Leu Leu Lys Gln Gly Gln Met Tyr Met Thr Asp Ser 380 385 390	1564
cag tgt act tcc aca ggc atg cca gtc cat atg caa agc cga tct atg Gln Cys Thr Ser Thr Gly Met Pro Val His Met Gln Ser Arg Ser Met 395 400 405	1612
tta aga cca ctg gag cta gcc tta cct aat caa gcc tca tat tcg gaa Leu Arg Pro Leu Glu Leu Ala Leu Pro Asn Gln Ala Ser Tyr Ser Glu 410 415 420	1660
aac gaa att tta aag aaa gaa tta gaa gca atg aga act ttc tgt gat Asn Glu Ile Leu Lys Lys Glu Leu Glu Ala Met Arg Thr Phe Cys Asp 425 430 435	1708
tca gca aaa caa gac aga ctc aaa ctc caa aat gaa ctg gct cac aag Ser Ala Lys Gln Asp Arg Leu Lys Leu Gln Asn Glu Leu Ala His Lys 440 445 450 455	1756
gtg gcg gag tgc aag gcc tta gca ttg gaa tgt gaa agg gtg aaa gag Val Ala Glu Cys Lys Ala Leu Ala Leu Glu Cys Glu Arg Val Lys Glu 460 465 470	1804
gat tca gat gag cag ata aag caa cta gaa gat gcc ttg aaa gac gtg Asp Ser Asp Glu Gln Ile Lys Gln Leu Glu Asp Ala Leu Lys Asp Val 475 480 485	1852
cag aag aga atg tat gag tcg gaa ggt aaa gtg aaa caa atg cag aca Gln Lys Arg Met Tyr Glu Ser Glu Gly Lys Val Lys Gln Met Gln Thr 490 495 500	1900
cat ttt ctt gcc ttg aaa gag cac ctg aca agt gat gcg gcc act ggg His Phe Leu Ala Leu Lys Glu His Leu Thr Ser Asp Ala Ala Thr Gly 505 510 515	1948
aac cac agg ctg atg gag gaa ctg aag gat cag ttg aaa gac atg aaa Asn His Arg Leu Met Glu Glu Leu Lys Asp Gln Leu Lys Asp Met Lys 520 525 530 535	1996
gtg aaa tac gaa ggt gcg tcc gca gaa gtg ggg aaa ttg aga aac caa Val Lys Tyr Glu Gly Ala Ser Ala Glu Val Gly Lys Leu Arg Asn Gln 540 545 550	2044
atc aaa caa aat gaa atg tta gtt gaa gag ttt aag aga gat gag ggc Ile Lys Gln Asn Glu Met Leu Val Glu Glu Phe Lys Arg Asp Glu Gly 555 560 565	2092

Fig. 4-3



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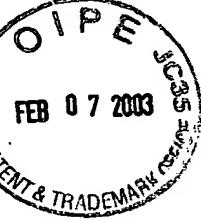
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aag ctg atg gaa gag aat aag cga ctg cag aag gag ttg agc atg tgt Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys 570 575 580	2140
gaa ctg gag cga gag aag aga gga agg aag ctc act gag atg gaa ggc Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly 585 590 595	2188
cag tta aag gac ttg tca gcc aag ctg gcc ctt tct att cca gca gag Gln Leu Lys Asp Leu Ser Ala Lys Leu Ala Leu Ser Ile Pro Ala Glu 600 605 610 615	2236
aaa ttt gaa aac atg aag agc ttg tta tca aat gaa ctg aac gag aag Lys Phe Glu Asn Met Lys Ser Leu Leu Ser Asn Glu Leu Asn Glu Lys 620 625 630	2284
gca aaa aaa tta ata gat gtg gaa aga gaa tat gaa aga tca ctt aat Ala Lys Lys Leu Ile Asp Val Glu Arg Glu Tyr Glu Arg Ser Leu Asn 635 640 645	2332
gaa act aga cca tta aag aga gaa ctt gag aat ttg aag gcc aaa ctg Glu Thr Arg Pro Leu Lys Arg Glu Leu Glu Asn Leu Lys Ala Lys Leu 650 655 660	2380
gct cag cac gtc aaa cca gag gaa cat gag cag ctc aag agc aga tta Ala Gln His Val Lys Pro Glu Glu His Glu Gln Leu Lys Ser Arg Leu 665 670 675	2428
gag cag aag tca gga gaa ctt ggg aag agg atc act gag tta aca tcg Glu Gln Lys Ser Gly Glu Leu Gly Lys Arg Ile Thr Glu Leu Thr Ser 680 685 690 695	2476
aaa aat cag acg tta caa aag gaa atc gaa aag gtc tgc ctg gat aat Lys Asn Gln Thr Leu Gln Lys Glu Ile Glu Lys Val Cys Leu Asp Asn 700 705 710	2524
aag ctc ctt aca caa caa gta aat aac tta aca act gaa atg aaa aat Lys Leu Leu Thr Gln Gln Val Asn Asn Leu Thr Thr Glu Met Lys Asn 715 720 725	2572
cat tac gtc cct tta aaa gta agt gaa gaa atg aaa aag tca cat gat His Tyr Val Pro Leu Lys Val Ser Glu Glu Met Lys Lys Ser His Asp 730 735 740	2620
gta att gtt gat gat ttg aat aaa aag ctt tca gat gtg aca cac aaa Val Ile Val Asp Asp Leu Asn Lys Lys Leu Ser Asp Val Thr His Lys 745 750 755	2668
tat aca gaa aag aag ttg gaa atg gag aag ttg ctt atg gaa aat gcc Tyr Thr Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Met Glu Asn Ala 760 765 770 775	2716

Fig. 4-4



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agt tta agt aaa aat gtc agc cgc ctg gaa act gtg ttc ata cct ccc	2764
Ser Leu Ser Lys Asn Val Ser Arg Leu Glu Thr Val Phe Ile Pro Pro	
780 785 790	
gag aga cac gaa aaa gaa atg atg gct ctg aaa tcc aat atc act gaa	2812
Glu Arg His Glu Lys Glu Met Met Ala Leu Lys Ser Asn Ile Thr Glu	
795 800 805	
ctt aag aag cag ctg tct gaa ctt aat aaa aaa tgt ggt gaa gac caa	2860
Leu Lys Lys Gln Leu Ser Glu Leu Asn Lys Lys Cys Gly Glu Asp Gln	
810 815 820	
gag aaa ata tat tca ctc atg tct gaa aac aat gat ttg aaa aag acc	2908
Glu Lys Ile Tyr Ser Leu Met Ser Glu Asn Asn Asp Leu Lys Lys Thr	
825 830 835	
atg agt cat cag tat gtg ccc gtg aaa acc cat gaa gag att aaa act	2956
Met Ser His Gln Tyr Val Pro Val Lys Thr His Glu Glu Ile Lys Thr	
840 845 850 855	
gcc ttg agt agc aca ttg gat aaa acc aat aga gaa tta gta gat gtg	3004
Ala Leu Ser Ser Thr Leu Asp Lys Thr Asn Arg Glu Leu Val Asp Val	
860 865 870	
aag aag aag tgt gaa gat ata aat caa gaa ttt gtg aaa ata aaa gat	3052
Lys Lys Lys Cys Glu Asp Ile Asn Gln Glu Phe Val Lys Ile Lys Asp	
875 880 885	
gag aac gaa ata tta aaa aga aat ctg gag aac act cag aac caa gta	3100
Glu Asn Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln Asn Gln Val	
890 895 900	
aaa gct gag tac atc agc cta aga gag cat gaa gaa aag atg agt ggc	3148
Lys Ala Glu Tyr Ile Ser Leu Arg Glu His Glu Glu Lys Met Ser Gly	
905 910 915	
cta agg aag agc atg aag aag gtc cag gac aac agc gct gaa ata ctg	3196
Leu Arg Lys Ser Met Lys Lys Val Gln Asp Asn Ser Ala Glu Ile Leu	
920 925 930 935	
gct aag tac aaa aaa agc cag gag gag att gtc acc ctg cat gag gag	3244
Ala Lys Tyr Lys Lys Ser Gln Glu Glu Ile Val Thr Leu His Glu Glu	
940 945 950	
att gca gcc cag aag aga gaa ctc gac acg ata cag gaa tgc atc aag	3292
Ile Ala Ala Gln Lys Arg Glu Leu Asp Thr Ile Gln Glu Cys Ile Lys	
955 960 965	
cta aaa tat gct ccg atc atc agc ttg gaa gag tgt gag aga aaa ttt	3340
Leu Lys Tyr Ala Pro Ile Ile Ser Leu Glu Glu Cys Glu Arg Lys Phe	
970 975 980	

Fig. 4-5



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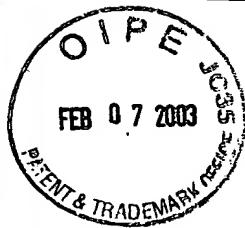
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aaa gcc act gag aaa gaa cta aaa gaa cag cta tcc cag cag aca cag Lys Ala Thr Glu Lys Glu Leu Lys Glu Gln Leu Ser Gln Gln Thr Gln 985 990 995	3388
aag tat aat acc agt gaa gaa gag gcc aag aag tgc aag caa gag aat Lys Tyr Asn Thr Ser Glu Glu Ala Lys Lys Cys Lys Gln Glu Asn 1000 1005 1010 1015	3436
gac aag tta aag aag gag atc ctc act ctt cag aag gat cta aag gat Asp Lys Leu Lys Lys Glu Ile Leu Thr Leu Gln Lys Asp Leu Lys Asp 1020 1025 1030	3484
aag aat gtt cac att gag aat tct tat gaa aca gaa aga gca tta agc Lys Asn Val His Ile Glu Asn Ser Tyr Glu Thr Glu Arg Ala Leu Ser 1035 1040 1045	3532
aga aaa aca gaa gag ctg aac aga cag tta aaa gac ctg ttg cag aaa Arg Lys Thr Glu Glu Leu Asn Arg Gln Leu Lys Asp Leu Leu Gln Lys 1050 1055 1060	3580
tac aca gag gca aag aag gag aaa gag aag ctc gtg gag gaa aat gcc Tyr Thr Glu Ala Lys Lys Glu Lys Glu Lys Leu Val Glu Glu Asn Ala 1065 1070 1075	3628
aag cag act tct gag atc ctt gca gca caa act ctt ttg cag aag cag Lys Gln Thr Ser Glu Ile Leu Ala Ala Gln Thr Leu Leu Gln Lys Gln 1080 1085 1090 1095	3676
cat gtt ccg ctg gag cag gtt gag tcc ctg aaa aaa tct ctt agt ggt His Val Pro Leu Glu Gln Val Glu Ser Leu Lys Lys Ser Leu Ser Gly 1100 1105 1110	3724
aca atc gag aca ctc aag gaa ctg aaa act aag cag aga tgt tat Thr Ile Glu Thr Leu Lys Glu Leu Lys Thr Lys Gln Arg Cys Tyr 1115 1120 1125	3772
gag aaa gag cag cag aca gtg acc caa ctg cgg cag atg ctg gag aat Glu Lys Glu Gln Gln Thr Val Thr Gln Leu Arg Gln Met Leu Glu Asn 1130 1135 1140	3820
cag aag aac tcc tct gtg ccc ctg gct gag cat ttg cag gtt aag gaa Gln Lys Asn Ser Ser Val Pro Leu Ala Glu His Leu Gln Val Lys Glu 1145 1150 1155	3868
gca ttt gag aaa gaa gtt gga atc ata aaa gct agc ttg aga gaa aag Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala Ser Leu Arg Glu Lys 1160 1165 1170 1175	3916
gaa gaa gaa agc caa aac aaa act gaa gag gtc tcc aaa ctc cag tct Glu Glu Glu Ser Gln Asn Lys Thr Glu Glu Val Ser Lys Leu Gln Ser 1180 1185 1190	3964

Fig. 4-6



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gag att cag aat act aaa caa gcg tta aaa aaa tta gag act cgg gag	4012
Glu Ile Gln Asn Thr Lys Gln Ala Leu Lys Lys Leu Glu Thr Arg Glu	
1195 1200 1205	
gtg gtt gat ttg tcg aaa tat aaa gca acg aaa agc gat ttg gag aca	4060
Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys Ser Asp Leu Glu Thr	
1210 1215 1220	
cag att tcc gac tta aac gaa aaa ttg gcc aat ctg aat agg aag tat	4108
Gln Ile Ser Asp Leu Asn Glu Lys Leu Ala Asn Leu Asn Arg Lys Tyr	
1225 1230 1235	
gag gaa gta tgt gag gag gtt ttg cat gcc aaa aag aag gaa ctg tct	4156
Glu Glu Val Cys Glu Glu Val Leu His Ala Lys Lys Lys Glu Leu Ser	
1240 1245 1250 1255	
gct aaa gat gag aag gaa ttg ctc cat ttc agc ata gag caa gaa atc	4204
Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser Ile Glu Gln Glu Ile	
1260 1265 1270	
aaa gat cag cag gaa cga tgt gac aaa tcc tta aca acc atc acg gag	4252
Lys Asp Gln Gln Glu Arg Cys Asp Lys Ser Leu Thr Thr Ile Thr Glu	
1275 1280 1285	
cta cag aga aga ata cag gaa tct gcc aaa caa atc gaa gca aaa gat	4300
Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln Ile Glu Ala Lys Asp	
1290 1295 1300	
aat aag ata act gaa ctg ctc aat gat gtg gag aga tta aaa cag gcc	4348
Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu Lys Gln Ala	
1305 1310 1315	
ctc aat ggc ctt tcc cag ctc acc tat gga agt ggg agt ccc agc aag	4396
Leu Asn Gly Leu Ser Gln Leu Thr Tyr Gly Ser Gly Ser Pro Ser Lys	
1320 1325 1330 1335	
agg cag agt cag ctg att gac agc ctg cag cag cag gtc agg tcc ctg	4444
Arg Gln Ser Gln Leu Ile Asp Ser Leu Gln Gln Gln Val Arg Ser Leu	
1340 1345 1350	
cag cag cag ctg gcg gat gcc gac aga cag cac caa gaa gta att gca	4492
Gln Gln Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu Val Ile Ala	
1355 1360 1365	
att tat cgg aca cac ctt ctt agt gct gca cag ggt cac atg gat gag	4540
Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln Gly His Met Asp Glu	
1370 1375 1380	
gat gtg cag gcc gcc tta ctg cag atc ata cag atg cgg cag ggg ctc	4588
Asp Val Gln Ala Ala Leu Leu Gln Ile Ile Gln Met Arg Gln Gly Leu	
1385 1390 1395	

Fig. 4-7



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gtg tgc tagtcggcac cccccagccc acagtggctt tccctgctgg tgctgagcat 4644
Val Cys
1400

tctgtgcgca acttcatggc ctttctgggc ctgcgtgtgc tagtataatt aaaataaagt 4704
gtatttgat ccatcaaaaa aaaaaaaaaa aa 4736

Fig. 4-8



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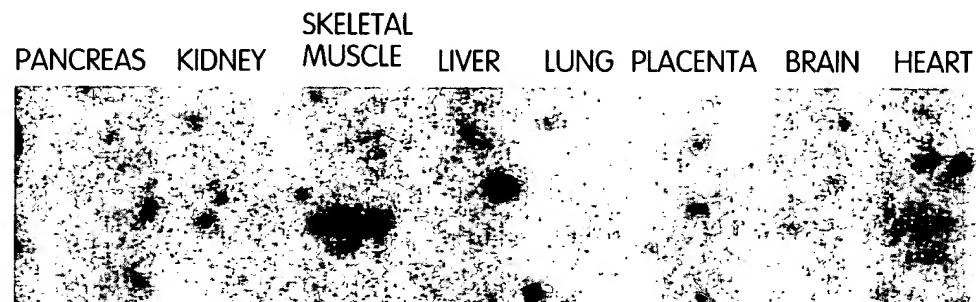


Fig. 5

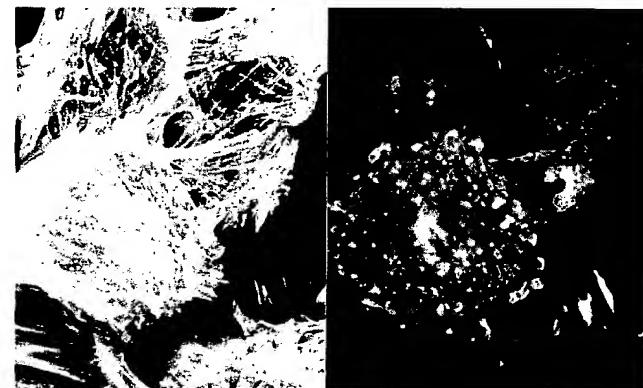


Fig. 6

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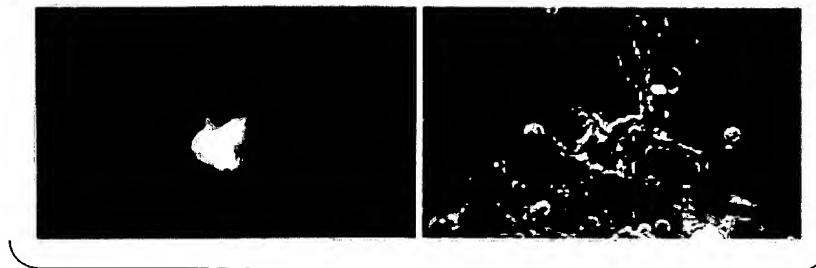


Fig. 7A

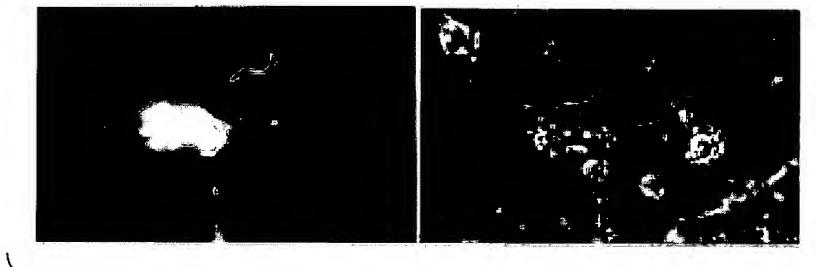


Fig. 7B

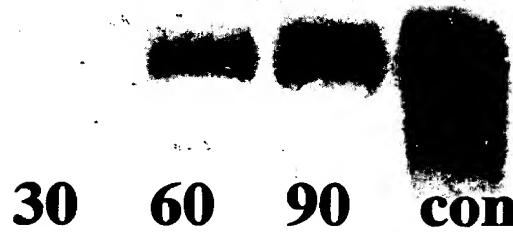


Fig. 8



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Sequence Alignment of bcap73 cDNA against Canine familiaris mRNA for C3VS protein
(GenBank accession X99145)

Query=βCAP73
Sbjct=C3VS

Query: 358 tttgctgttagcaacaagaaaactaaatccgtctatgatgagctgtgggtttttgtgc 417

Sbjct: 12 tttgctgttagcaaccagaaacccaaatccgtctatgatgaaactgtgggtttttgtgc 71

Query: 418 tcctaagaacagacaaggcaggatggaaacaaatacgatgaccgattgatgagaggcgc 477

Sbjct: 72 tcctaagaacagacaatgcaggatggaaacaaatcgatgaccgattgatgaaaggccgc 131

Query: 478 agaaaaggggagatgttagaaaaagtgtcctcaatcctgtctaaaaaggagtcataatccagg 537

Sbjct: 132 ggagagggggagatgttagaaaaagtgtcctcaatcctgtctaaaaaggcatcaatccagg 191

Query: 538 caagcttagatgttagaaggcagatctgccttcatgttgcggctcaaaggaaatcttga 597

Sbjct: 192 caaacttagatgtggaaaggcagatctgcctccatgttgcggctcaaaggaaatcttga 251

Query: 598 gtgtttgaatgccatcctcatacatggagttgatattacaaccagtgcacccgcaggaag 657

Sbjct: 252 atgtttgaatgccatccttatacatggagttgatattacaaccagtgcacactgcaggaaag 311

Query: 658 gaatgctcttacacctggctgcaaagtatggcatgcactgtgtctacaaaaaacttctaca 717

Sbjct: 312 aaatgctcttacacctggctgcaaagtatggcatgcattgtgtctacaaaaaacttctaca 371

Query: 718 gtacaattgtcccactgaacatgttagacacctgcaggaaagaactgcacttcatgtgcagc 777

Sbjct: 372 gtacaattgtcccactgaacatgtcagacctgcaggaaagaaccgcacttcatgcacgc 431

Query: 778 tatggcagactgtccttctagcatacagctgtctgcgaccatggggcctcggtgaatgc 837

Sbjct: 432 aatggcagactgtccttccagcatacagctgtcttgcattgtgaccatggggcctccgtgaatgc 491

Query: 838 caaagatgttagatggcgacaccacttggctggctaccagatgtgttaggccaacaat 897

Sbjct: 492 caaagatgtggatggcgacaccgtggctggctactcagatgtgttaggccaacaat 551

Fig. 9-1

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Query: 898 atgtcaactgctgatagatagagggcggatattaattccagagacaaacaaaacaggac 957
Sbjct: 552 ctgtcaactgctgatagatcgagggcagagattaattccagagacaaacaaaacagaac 611

Query: 958 tgctctcatgcttaggatgcgagtatggtgcaaagatgcagtagaagtcttaatcaaaaa 1017
Sbjct: 612 tgctctcatgctgggtgcgagtatggtgtaaggatgctgtagaagtcttacttaaaaa 671

Query: 1018 cggcgctgacgtgaccttgctggacgcgcctggccatgacagttcttactatgcaagaat 1077
Sbjct: 672 tggtgctgatgtaaacgcctgctggatgcctggccatgatagttcttactatgcaagaat 731

Query: 1078 tggtgacaatctggacattctaacccttactgaagactgcatacagaaaattccaacaaagg 1137
Sbjct: 732 tggtgacaatctggacattctaactttattgaagactgcgtcagaaaatccaacaaagg 791

Query: 1138 gagagaactttgaaagaaaggaccatcttacaacacagcgaatttgcagatgctaga 1197
Sbjct: 792 gagagaactttgaaagaaaggaccatcttacagcagcgaatttgcgtacatgctaga 851

Query: 1198 tgaagtaaatcgaagtcaaatcagagggagcatcaaacattcaggatctggagattga 1257
Sbjct: 852 tgaagtaaatgtgaagtcaagtcagagggagcatcgaacattcaggagctggagattga 911

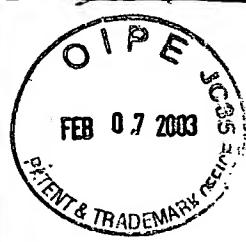
Query: 1258 aaatgaagatctgaaagagagattgagaaaaattcagcaagaacagagaatattttgga 1317
Sbjct: 912 aaatgaagattgaaagacaggttgagaaaaattcagcaagaacagagaatattactgga 971

Query: 1318 taaagtcaatggttacagctacagctgaatgaggaagtaatggtggtgatctgga 1377
Sbjct: 972 taaagtcaatggttacaactacagctgaatgaggaagtgatggtggtgatctgga 1031

Query: 1378 aagtgagaaaagaaaagctgaagtccctttggcagccaaagaaaagcagcatgaagaaag 1437
Sbjct: 1032 aagtgagaaaagaaaagctgaagtctttggctaaagaaaagcaacatgaagaaag 1091

Query: 1438 cctaagaactattgaggctctgaaaagttagatttaagtatttgag 1483
Sbjct: 1092 cctaagaactattgaggctctgaaaaacagattaaatatttgag 1137

Fig. 9-2



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Query: 1566 agtgtacttccacaggcatgccagtccatatgcaaagccatctatgttaagaccactgg 1625

Sbjct: 1136 agtgtactccccaggggtgccagccacatgcaaagcaggtctatgttaagaccactgg 1195

Query: 1626 agctagccttacctaattcaagcctcatattcgaaaacgaaatttaaagaaagaattag 1685

Sbjct: 1196 agctatcattaccatcaaaccctcatattctgaaaatgacctttaaagaaagagttag 1255

Query: 1686 aagcaatgagaactttctgtgattcagcaaaacaagacagactcaaactccaaaatgaac 1745

Sbjct: 1256 aagcaatgagaactttctgcgaatcagccaaacaagaccgcctcaagctccagaacggag 1315

Query: 1746 tggctcacaagggtggcgagtgcaaggccttagcattggaatgtgaaagggtgaaagagg 1805

Sbjct: 1316 tggcgcacaagggtggctgagtgcaagctttaggacttagaatgtgaacgcattcaaggagg 1375

Query: 1806 attcagatgagcagataaagcaactagaagatgccttggaaagacgtgcagaagagaatgt 1865

Sbjct: 1376 actctgtatgagcagataaagcagtttagaaagacgcattggaaagatgtgcagaagagaatgt 1435

Query: 1866 atgagtcggaaggtaaagtgaaacaaatgcagacacatttcttgccttggaaagacgcacc 1925

Sbjct: 1436 atgagtcggaaggtaaagtaaaacaaatgcagacacactttcttgccttggaaagacgcacc 1495

Query: 1926 tgacaagtgtgcggccactggaaaccacaggctgtatggaggaactgaaggatcagttga 1985

Sbjct: 1496 tgaccagtgtaaagcagctatggaaatcacagactaatggaggagctgtggaaaggatcagttga 1555

Query: 1986 aagacatgaaagtgaaatacgaagggtgcgtccgcagaagtggggaaattgagaaaccaa 2045

Sbjct: 1556 aggacatgaaagcgaatatgagggtgcattcagcagaagtggaaaactgcgaaaccaa 1615

Query: 2046 tcaaacaaaatgaaatgttagttgaagagtttaagagagatgaggggcaagctgtatggaa 2105

Sbjct: 1616 tcaaacaaaatgagctgttagtgcatacagtttaggagagatgtggaaaggcaagctgggtggaa 1675

Query: 2106 agaataagcgactgcagaaggagggtgagcatgtgtgaactggagcgagagaagagagggaa 2165

Sbjct: 1676 agaataagcgattgcagaaggactcgtatgtgtgaaacggagcgagacaagaaaggaa 1735

Fig. 9-3



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Query: 2166 ggaagctcaactgagatggaaggccagttaaaggacttgtcagccaaagctggcccttcta 2225

Sbjct: 1736 ggagggttgctgaggtgaaaggccaggtaaaggaactcttagcaaagctgaccttgtcag 1795

Query: 2226 ttccagcagagaaaattgaaaacatgaagagcttgttatcaa 2267

Sbjct: 1796 ttccaaactgaaaaattttagagcatgaagagcttattatcaa 1837

Fig. 9-4



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Sequence Alignment of bcap73 against Tentative Human Concensus (THC) Contiguous Sequences
THC244788 THC143090 THC186491 THC213238 (from TIGR)

Score = 1052 bits (547), Expect = 0.0

Identities = 905/1092 (82%), Positives = 905/1092 (82%), Gaps = 4/1092 (0%)

Query=bcap73 cDNA

Sbjct=THC seq

Query: 3136 aaagatgagtggcctaaggaagagcatgaagaaggccaggacaacagcgctgaaatact 3195

Sbjct: 6 aaagatgagctcgctaagtcagacatgagaaaggtsaggatagtaatgctgaaatctt 65

Query: 3196 ggctaagtacnnnnnnngccaggaggattgtcaccctgcatgaggagattgcagccca 3255

Sbjct: 66 ggccamctacagaaaaggccaagaagagattgtgacactkcatgccgaaattaragccca 125

Query: 3256 gaagagagaactcgacacgatacaggaatgcatcaagctaaatatgctccgatcatcg 3315

Sbjct: 126 gargaraggctcgacacaatacaagartgcattaaggtaaaatatgccccattgtcag 185

Query: 3316 ctggaaagagtgtgagagaaaatttaaagccactgagaaagaac-taaaagaacagctat 3374

Sbjct: 186 ctttggaggatcscgagagaaaatttaaagcaacagagaaagaacctaaggatgttat 245

Query: 3375 cccagcagacacagaagtataataccagtgaagaagaggccaagaagtgcaccaagaga 3434

Sbjct: 246 cagagcagacacaaaagtatagtgtcagtgcattaaggtaaaaaacaagcaagaga 305

Query: 3435 atgacaagttaaagaaggagatcctcactcttcagaaggatctaaaggataagaatgttc 3494

Sbjct: 306 atgacaagttaaagaaggagattttacccttcagaaggatgtgagagayaagacatgttc 365

Query: 3495 acattgagaattcttatgaaacagaaagagcattaaggcagaaaaacagaagagctgaaca 3554

Sbjct: 366 tcattgagaagtctcatgaaatggaaagagcattaaggcagaaaaacagacgagctaaaca 425

Query: 3555 gacagttaaaagacctgttcagaaatacacagaggccaaagaaggagaaagagaagctcg 3614

Sbjct: 426 aacagttaaaagacttgtcacagaaatacacggaaatgtgaaagagaagctag 485

Fig. 10-1



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Query: 3615 tggaggaaaatgccaaggcagacttctgagatcctgcagcacaaaactctttgcagaagc 3674

Sbjct: 486 tagaagaaaatgccaacacagacttctgagatacttgcaactgcaggcaaaaatctttgcaaaaac 545

Query: 3675 agcatgttccgctggaggcaggttgagtccctgaaaaaatctcttagtggtacaatcgaga 3734

Sbjct: 546 aacatgttccatttggAACAGGTTGAGGCTCTgaaaaaatctcttaatggcacaattgaaa 605

Query: 3735 cactcaaggagaactgaaaactaaggcagagatgttatgagaagagcagcagacagtga 3794

Sbjct: 606 atctaaaggagaactgaagagatgtcaaagggtttacgagaagagcagcagacagtga 665

Query: 3795 cccaaactgcggcagatgctggagaatcagaagaactcctctgtgcccctggctgaggcatt 3854

Sbjct: 666 cccaaactgcattttttggagaatcaaaagaactcttctgttacccctggcagagcatt 725

Query: 3855 tgcaggtaaggaagcatttgagaaagaagttggaatcataaaagcttagttgagagaaa 3914

Sbjct: 726 tgcagattaaagaagcatttgagaaagaagttggaatcataaaagccagcttggagagaaa 785

Query: 3915 aggaagaagaaagccaaaacaaaactgaagaggtctccaaactccagtctgagattcaga 3974

Sbjct: 786 aggaagaagaaagccaaaacaaaatggagaagtctccaaacttcagtcggaggttcaga 845

Query: 3975 atactaaacaagcgtnnnnnnnnttagagactcggaggtggattgtcgaaatata 4034

Sbjct: 846 atactaaacaagcmtaaaaatttagagacttagagaggttagttgacttgcataatata 905

Query: 4035 aagcaacgaaaagcgatttgagacacagattccgacttaacgaaaaattggccaatc 4094

Sbjct: 906 aagcaacaaaaagtgtttggagacacagattctagcttaatgaaaaattggccaatc 965

Query: 4095 tgaataggaagtatgaggaagtatgtgaggagtttgcatgcaaaaagaaggaactgt 4154

Sbjct: 966 tgaatagaaagtatgaggaagt-tgtgaggagtttgcatgcccmaaaagaaggaaat 1024

Query: 4155 ctgctaaagatgagaaggattgctccatttcagcatagagcaagaaatcaaagatcagc 4214

Sbjct: 1025 ctgscaaagatgagaagga-ttactgc-tttcaccttggscagaaaattaagggtcagr 1082

Fig. 10-2



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TECH CENTER 1600/2900

19/19

Query: 4215 aggaacgatgtg 4226

Shift 1003 Assessment

Sbjct: 1083 aggaacgatgtg 1094

Fig. 10-3